

# Estimation of Heritability of Mastitis Disease Using ANOVA Method

Subrat Keshori Behera<sup>\*</sup>, A K Paul<sup>\*\*</sup> and S D Wahi<sup>\*\*\*</sup>

Mastitis disease being a threshold character in dairy cattle breeding, needs an in-depth study especially with regard to its inheritance. The Analysis of Variance (ANOVA) estimator method and a modified method given by Fleiss were applied to find the heritability of mastitis disease. The concept of intraclass correlation coefficients was used in calculating the heritability. The results obtained showed similarity with the results cited in literatures.

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**Keywords:** Heritability, Intraclass correlation, Mastitis disease, Threshold character

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## Introduction

There are many characteristics of economic importance in animal and plant breeding which are polygenic in inheritance but their phenotypic expressions show discontinuity. The characters are expressed in 'all or none' fashion. Although they lack a continuous distribution, such characters are known to be multifactorial in their inheritance. The relationship between polygenes and the expression of such characters come about through the establishment of 'thresholds'. Thus, there are two separate scales for the description of the phenotypic values. The underlying polygenic distribution which is continuous and the visible phenotypic distribution which is discontinuous and the two scales are connected by a 'threshold'—a point of discontinuity. Thus, the heritabilities of these important traits should be obtained by an alternative technique rather than the classical methods employed for continuous traits. Dempster and Lerner (1950) and Bhatia *et al.* (1992) developed an algorithm for calculating the heritability of such binary traits and further Gianola (1979) generalized it. Van Vleck (1980) used the algorithm in a simulation study of sib and parent offspring analysis of binary trait. Magnussen and Kremer (1995) considered the beta-binomial model for estimating the heritability of binary trait in plant breeding using the concept of selection response and realized heritability. Ridout *et al.* (1999) reviewed different estimators of intraclass correlation for binary data and compared them in an extensive simulation study. Here, in the present investigation, live data are used for the estimation of heritability of mastitis disease in the case of Sahiwal breed of cows through estimation of intraclass correlation coefficient. The intraclass correlation coefficient provides a quantitative measure of similarity between individuals within groups.

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<sup>\*</sup> Research Associate, Indian Agricultural Statistics Research Institute, New Delhi 110012, India.  
E-mail: subrat.iasri@gmail.com

<sup>\*\*</sup> Senior Scientist, Indian Agricultural Statistics Research Institute, New Delhi 110012, India; and is the corresponding author. E-mail: apaul\_66@yahoo.com

<sup>\*\*\*</sup> Principal Scientist, Indian Agricultural Statistics Research Institute, New Delhi 110012, India.  
E-mail: sdwahi@iasri.res.in

## Methodology

Suppose the  $i^{\text{th}}$  sire ( $i = 1, 2, \dots, k$ ) is made to mate with a set of  $n_i$  dams selected at random giving rise to one progeny each. Consider the random linear model,

$$X_{ij} = \mu + s_i + e_{ij}$$

where  $X_{ij}$  is the observation on the progeny of  $j^{\text{th}}$  ( $j = 1, 2, \dots, n_i$ ) dam which is mated with the  $i^{\text{th}}$  sire ( $i = 1, 2, \dots, k$ ),  $\mu$  is the general mean,  $s_i$  is the effect of the  $i^{\text{th}}$  sire and  $e_{ij}$  is the uncontrolled environmental and genetic deviations attributable to individuals within the sire groups. All effects are assumed to be at random with

$$E(s_i) = E(e_{ij}) = 0, E(s_i^2) = \sigma_s^2 \text{ and } E(e_{ij}^2) = \sigma_e^2$$

The Analysis of Variance (ANOVA) based on this model is shown in Table 1.

| SV            | df      | SS     | MSS    | E(MS)                            |
|---------------|---------|--------|--------|----------------------------------|
| Between sires | $k - 1$ | $SS_b$ | $MS_b$ | $\sigma_e^2 + \lambda\sigma_s^2$ |
| Within sires  | $N - k$ | $SS_w$ | $MS_w$ | $\sigma_e^2$                     |

The estimator is given by:

$$\hat{\rho}_{AOV} = \frac{MS_b - MS_w}{MS_b + (\lambda - 1)MS_w}$$

where  $MS_b$  and  $MS_w$  are, respectively, the between-group and within-group mean squares from a one-way ANOVA of the binary data  $X_{ij}$  and where

$$\lambda = \frac{1}{k-1} \left[ N - \sum_{i=1}^k \frac{n_i^2}{N} \right] \text{ with } N = \sum_{i=1}^k n_i$$

For binary data, explicit formulas for  $MS_b$  and  $MS_w$  are:

$$MS_b = \frac{1}{k-1} \left[ \sum_{i=1}^k \frac{Y_i^2}{n_i} - \frac{1}{N} \left( \sum_{i=1}^k Y_i \right)^2 \right]$$

Fleiss (1981) used a modification of this estimator, which is denoted by  $\hat{\rho}_{AOV}^*$ , in which the divisor of  $MS_b$  is  $k$  rather than  $(k - 1)$ .

So,

$$\hat{\rho}_{AOV}^* = \frac{MS_b - MS_w}{MS_b + (\lambda - 1)MS_w}$$

where,

$$MS_b = \frac{1}{k} \left[ \sum_{i=1}^k \frac{Y_i^2}{n_i} - \frac{1}{N} \left( \sum_{i=1}^k Y_i \right)^2 \right]$$

### Estimation of Heritability Using Intraclass Correlation Coefficient

The half-sib heritability estimate will be obtained by the formula

$$\hat{h}^2 = 4 \times \hat{\rho}$$

where  $\hat{\rho}$  is the estimated intraclass correlation coefficient.

### Estimation of Standard Error

According to Falconer (1998), Standard Error for half-sib heritability estimate can be obtained by the formula

$$\text{Standard Error} = 32 \frac{\hat{h}^2}{T}$$

where  $T = nN$  and  $n$  is average half-sib family size,  $N$  is the number of half-sib family size. As an exact formula for standard error for unbalanced situation is not available, the above approximate formula has been used for this study.

### SAS Code for Estimation of Heritability

(i) SAS program for the estimation of heritability and its standard error through calculation of intraclass correlation coefficient by a method based on  $P_{AOV}$  is given below:

```
data test;
input ni yi;
datalines;
52 19
18 6
.....
.....

;
proc print data = test;
```

```

proc iml;
use test;
read all var{n} into n;
read all var{y} into y;
k = nrow(n);
N = n{+,};
n_i p n_i = n_i * n;
n0 = (1/(k-1))*(N-(n_i p n_i / N));
totaly_i = y_i{+,};
sum1 = 0;
do i = 1 to k;
sum1 = sum1 + (y_i[i,]*y_i[i,] / n_i[i,]);
end;
MS_b = (1/(k-1))*(sum1-(totaly_i*totaly_i/N));
MS_w = (1/(N-k))*(totaly_i-sum1);
Ro = (MS_b-MS_w)/(MS_b+(n0-1)*MS_w);
h^2 = Ro*4;
SE = (32*h^2)/((N/k)*k);
print N n_i p n_i n0 totaly_i sum1 MS_b MS_w Ro h^2 SE;
run;

```

(ii) SAS program for estimation of heritability and its standard error through calculation of intraclass correlation coefficient by a method based on  $\rho_{AOV}$  is given below:

```

data test;
input n_i y_i;
datalines;
52 19
18 6
.....
.....

```

```

;
proc print data = test;
proc iml;
use test;
read all var{n} into n;
read all var{y} into y;
k = nrow(n);
N = n{+,};
n_i_rho_n_i = n_i{*}n_i;
n0 = (1/(k-1))*(N-(n_i_rho_n_i/N));
totaly_i = y_i{+,};
sum1 = 0;
do i = 1 to k;
sum1 = sum1 + (y_i[i,]*y_i[i,]/n_i[i,]);
end;
MS_b = (1/k)*(sum1-(totaly_i*totaly_i/N));
MS_w = (1/(N-k))*(totaly_i-sum1);
Ro = (MS_b-MS_w)/(MS_b+(n0-1)*MS_w);
h^2 = Ro*4;
SE = (32*h^2)/((N/k)*k);
print N n_i_rho_n_i n0 totaly_i sum1 MS_b MS_w Ro h^2 SE;
run;

```

### Data Description

The data was collected from breeding farm of Sahiwal cows, National Dairy Research Institute (NDRI), Karnal. There were 86 sires with 1,422 progenies, out of which 474 were affected by mastitis. Here in the data, '0' indicates resistance to the disease and '1' indicates the appearance of disease.

### Results

Using the developed SAS programs, we have calculated the required intraclass correlation coefficients, heritability estimates and their standard errors which are as follows:

By ANOVA estimator method, we have calculated  $\hat{\rho}_{AOV}$  equals to 0.0061. From this, we have calculated  $\hat{h}^2$  value equals to 0.0244 and its standard error equals to 0.0005. By the Fleiss (1981) method, we have calculated  $\hat{\rho}_{AOV}^*$  equal to 0.0053. And from this we calculated the  $\hat{h}^2$  value, which is equal to 0.0213 with its standard error equal to 0.0004. The results are in agreement with the heritability estimates of mastitis disease (0.02 to 0.04) obtained by Weller *et al.* (1997).

### Conclusion

The intraclass correlation coefficients obtained in the study matched well with the heritability estimates of mastitis disease found in the literature. ❁

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